

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 15, 2004, 09:22:37 ; Search time 2144.55 seconds
(without alignments)
6739.548 Million cell updates/sec

Title: US-09-973-674A-16
Perfect score: 484
Sequence: 1 atgcgaattggacacgggttt.....taaggcaacaaatgattga 484

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pin.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gsl.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	261.2	54.0	520	13	C14748
C 2	260.6	53.8	699	28	AQ990151
C 3	225.4	46.6	464	14	D80872
C 4	186.4	38.5	593	28	BZ351818
					C14748 C14748 Clon
					AQ990151 Rfc00873
					D80872 HUM13A12A
					BZ351818 hx72g05.g

5	184.4	38.1	654	28	BZ423610
6	138.4	28.6	1350	28	BZ567684
7	137	26.3	800	28	AQ991620
C 8	128	26.4	370	13	C15063
9	126.4	26.1	577	28	AQ242254
C 10	123	25.4	305	10	BF633873
C 11	123	25.4	305	10	BF633873
C 12	122.4	25.3	642	12	BF634326
13	121	25.0	773	13	BF634326
C 14	120	24.8	834	28	BF634326
15	119	24.6	811	28	BF634326
16	116.6	24.1	615	12	BF634326
17	116	24.0	527	9	AV394739
C 18	115	23.8	670	13	BQ796553
C 19	115	23.8	794	13	BQ800490
C 20	113.6	23.5	709	12	B1406315
C 21	112.6	23.3	695	9	AV783270
22	112	23.1	471	9	AV624871
23	112	23.1	489	9	AV620733
24	112	23.1	513	9	AV624394
25	111.2	23.0	581	28	BZ567684
C 26	111	22.9	560	9	AI670587
C 27	111	22.9	604	9	AI712133
28	110.4	22.8	812	14	CF668118
29	109.4	22.6	717	14	CF628504
C 30	108.6	22.4	523	13	BU765979
C 31	108.6	22.4	598	11	AY110686
32	108.6	22.4	770	14	CD574682
C 33	107.8	22.3	617	13	BU550772
C 34	107.2	22.1	693	14	CF475706
35	107	22.1	747	14	CF830014
36	107	22.1	765	14	CA783831
C 37	107	22.1	836	14	CF832762
C 38	107	22.1	843	14	CF832760
C 39	107	22.1	849	14	CF836632
40	105.4	21.8	615	14	CF811207
41	105.4	21.8	666	9	AV822490
42	105.4	21.8	732	12	BM658076
C 43	105	21.7	668	10	AW309700
44	104.6	21.6	661	12	BG129487
C 45	104.6	21.6	1106	14	CK215381

ALIGNMENTS

RESULT 1
C14748/c
LOCUS
DEFINITION
C14748 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA
clone GEN-086802 3', mRNA sequence.
ACCESSION
C14748
VERSION
C14748.1 GI:1569455
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
C14748 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA
clone GEN-086802 3', mRNA sequence.

AUTHORS
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.
TITLE
Fujiwara et al. (1995)
JOURNAL
Unpublished (1995)
COMMENT
Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.

FEATURES
source
1..520

/clone lib="WGS-SbicolorF (DH5a methyl filtered)"
 /note="Site 1: Xba I; Site 2: Xba I; The vector was
 digested with XbaI and one nucleotide was added by fill in
 in the recessive 3' end. The genomic DNA was nebulized,
 end repaired, adaptor ligated and size fractionated using
 sephadex. The resulting fragments were between 0.8 and 3
 kb and were cloned into the vector (.x/y reads in M13mp19,
 b/g reads in pUC19). The same ligation was transformed
 into DH5a."

ORIGIN

```

Query Match      38.1%; Score 184.4; DB 28; Length 654;
Best Local Similarity 80.8%; Pred. No. 1.8e-38;
Matches 215; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 ATGCGAATTGACACGGTTTTCAGCTATCGCTTTGGCGGTGAAGGCCCAATTATCATTT 60
Db ATGCGTATCGGTACGGTTTTCAGCTATCGCTTTGGCGGTGAAGGCCCAATTATCATTT 441
QY 61 GGTGCGGTACGATTCCTTACGAAAGGATTGCTGGCGGATTCCTGATGGCGACGTGGCG 120
Db GCGCGGGTGGCGATTCCTTACGAAAGGATTGCTGGCGGATTCCTGATGGCGACGTGGCG 501
QY 121 CTCATGCGTTGACCGATGCAATTTGCTGGCGGCGGCTGGCGGATTCGCGCAAGCTG 180
Db CTGATGCGTACCGACGCGCTGCTGGCGGCGGCTGGCGGATTCGCGCAAGCTG 561
QY 181 TTCGCGGATACGATTCGCGCAATTTAAAGTGGCGATAGCCGCGAGCTGTCAGCGAAGCC 240
Db TTCGCGGACCGATTCGCGCAATTTAAAGTGGCGGCGGCTGGCGGATTCGCGCAAGCC 621
QY 241 TGGCGTTCGATTCAGCGCAAGGTTTATACCTTTGGCAAGCTGCTCACTATCATGCT 266
Db TGGCGTTCGATTCAGCGCAAGGTTTATACCTTTGGCAAGGCTA 647

```

RESULT 6

```

BZ567684
LOCUS pacs2-164_7159.xl pacs2-164 Pseudomonas aeruginosa genomic clone
DEFINITION pacs2-164_7159, genomic survey sequence.
ACCESSION BZ567684
VERSION BZ567684.1 GI:27199364
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE 1 (bases 1 to 1350)
AUTHORS Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
JOURNAL J. Bacteriol. (2002) In press
COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
Location/Qualifiers
1. .1350
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="2-164"
/db_xref="taxon:287"
/clone="pacs2-164_7159"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
library."

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FEATURES

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source
1. .1350
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="2-164"
/db_xref="taxon:287"
/clone="pacs2-164_7159"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
library."

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ORIGIN

```

Query Match      28.6%; Score 138.4; DB 28; Length 1350;
Best Local Similarity 58.0%; Pred. No. 4.7e-26;
Matches 244; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 1 ATGCGAATTGACACGGTTTTCAGCTATCGCTTTGGCGGTGAAGGCCCAATTATCATTT 60
Db ATGCAACTCGGCGCATGGTTTACACGTGATCGCTTCGCGGAGGGCGACTTGATCACCCCTC 233
QY 61 GGTGCGGTACGATTCCTTACGAAAGGATTGCTGGCGGATTCCTGATGGCGACGTGGCG 120
Db GCGGAGTGGCGATTCGCCACAACATGGCTGGTGGCCACTCTCTACGGAGACGTGGCTG 293
QY 121 CTCATGCGTTGACCGATGCAATTTGCTGGCGGCGGCTGGCGGATTCGCGCAAGCTG 180
Db CTGACAGCGCTTGTCCGATGCGCTCTCGCGCGGCGCATCTCTGCGCGACATCTTCTAGCAC 353
QY 181 TTCGCGGATACGATTCGCGCAATTTAAAGTGGCGGATAGCCGCGAGCTGTCAGCGAAGCC 240
Db TCTCGGCACACCGACCGCTGGTTCAAGGGCTCTCTACGTGCGCGCTGGTGGCGACACGTG 413
QY 241 TGGCGTTCGATTCAGCGCAAGGTTTATACCTTTGGCAAGCTGCTCACTATCATGCT 300
Db ATGCGCATGCTGGCGAGCGCTGGCTGAAGGTTGGCAAGCTCTACGCCACATTTGCGTCT 473
QY 301 CAGGCACCGAAGATGTTGCGCACATTCACAAATCCGCGTGTATTATTCGCGAAGATCTC 360
Db CATGCGCGCAAGATGGCTCGGACATCGAGACCATGAGCGGTTGATCGCCAAGGACCAT 533
QY 361 GCGTCCCATATGATGATGTTAACTGAAGCCACTACTACGGAAGAACTGGGATTTACC 420
Db TCGGTNTTGAAGCATGAGCTGAACGTCTTGCCCAACCATCTCTCGAGAGGCTTGTATAACC 593
QY 421 G 421
Db 594 G 594

```

RESULT 7

```

AQ991620
LOCUS Rf01133F Photorhabdus luminescens strain W14 M13 library
DEFINITION Photorhabdus luminescens genomic clone PLG01133F, genomic survey
sequence.
ACCESSION AQ991620
VERSION AQ991620.1 GI:9650289
KEYWORDS GSS.
SOURCE Photorhabdus luminescens
ORGANISM Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 800)
AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsr@bath.ac.uk
This is one of a selected subset of flipped clones from the M13
library. For annotation of identified clones (BIASIX, BLASTN and
mapping to E. coli K12 genome) please see ffrench-Constant et al.
2000, Nucleic Acids Res.
Seq primer: M13 Reverse
Class: shotgun.
Location/Qualifiers

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source
1. .800
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01133F"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13 library"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
Query Match
Best Local Similarity 28.3%; Score 137; DB 28; Length 800;
Matches 182; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 214 GATAGCCGAGCTGCTAGCGAAGCTGCGCTGCTGATTCAGCGAAGGTTATACCTT 273
DB 30 GATAGCCGTAATATTGCGGAAGCTATTACGCTATCANAGAAAGGTTATCGATT 89
QY 274 GSCAAGCTCGATGCTACATATCATGCTCAGGACCGAAGATGTCGCGACATTCACAA 333
DB 90 GCAATCTTGATATTACGATATTCGCTCAAGCACCCAAATGCTCGCATATTCCAA 149
QY 334 ATGCGCGTGTATTGCGCAAGATCTGCGCTGCCATATGATGATGTTAACTGAAAGCC 393
DB 150 ATGAGAGTCAATCTGCGAAGATCTACATGCCACATGATGATCAATGTTAAAGCC 209
QY 394 ACTACTACGGAAGAACTGGGATTTACCGAGCTGGGAGGAGGATTCCTGTGAACGGTG 453
DB 210 ACAACTACGGAATATTAGGATTTGTTGGCGTAAAGAGGTATTGCTTGGAGCAAGTT 269
QY 454 GCGCTACTCATTAAAGCA 471
DB 270 GCTTGTGCTGTTAAGGAA 287

RESULT 8
C15063/c
LOCUS
DEFINITION
C15063 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA
clone GEN-113F02 3', mRNA sequence.
ACCESSION
C15063
VERSION
C15063.1 GI:1569770
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 370)
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,
Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.,
Maekawa, H., Shin, S. and Nakamura, Y.
Fujiwara et al. (1995)
Unpublished (1995)
CONTACT: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.

FEATURES
source
1..370
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GEN-113F02"
/clone_lib="Clontech human aorta polyA+ mRNA (#6572)"

ORIGIN
Query Match
26.4%; Score 128; DB 13; Length 370;

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Best Local Similarity 95.6%; Pred. No. 1.7e-23;
Matches 151; Conservative 2; Mismatches 3; Indels 3; Gaps 2;

QY 327 TCACAAATGCGCGTGTATTATTCGCGAAGATCTCGGCTGCCATATGGATGATGTTAACCT 386
DB 368 TCACAAATGCGCGTGTATTATTCGCGAAGATCTCGGCTGCCATATGGATGATGTTAACCT 309
QY 387 GAAAGCCACTACTACGGAAGAACTGGGATTTACCGAGCTGGGAGGAGGATTCCTGTGA 446
DB 308 GAAAGCCACTACTACGGAAGAA--CTGGATTTACCGAGCT--GGGAAGGATTCCTGTGA 252
QY 447 AGCGTGGCGTACTCATTAAAGCAACAAATGATTGA 484
DB 251 AGCGTGGCGTACTCATTAAAGCAACAAATGATTGA 214

RESULT 9
AQ242254
LOCUS
DEFINITION
3P02-39r Ochrobactrum anthropi BAC Library Ochrobactrum anthropi
genomic clone 3P02-39r, genomic survey sequence.
ACCESSION
AQ242254
VERSION
AQ242254.1 GI:3688053
KEYWORDS
GSS.
SOURCE
Ochrobactrum anthropi
ORGANISM
Ochrobactrum anthropi
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Ochrobactrum.
REFERENCE
1 (bases 1 to 577)
Tomkins, J., Miller-Smith, H., Sasinowski, M., Choi, W., Sasinowska, H.,
Verce, M., Freedman, D., Dean, R. and Wing, R.A.
Physical map and gene survey of the Ochrobactrum anthropi genome
using bacterial artificial chromosome contigs
Microb. Comp. Genomics 4 (3), 203-217 (1999)
20055259
10587947
PUBMED
COMMENT
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Class: BAC ends
High quality sequence stop: 1.
Location/Qualifiers
1..577
/organism="Ochrobactrum anthropi"
/mol_type="genomic DNA"
/db_xref="taxon:529"
/clone="3P02-39r"
/lab_host="DH10B E. coli"
/clone_lib="Ochrobactrum anthropi BAC Library"
/note="Vector: pBelosAC11; Site 1: HindIII; Site 2:
HindIII; Ochrobactrum anthropi is an important microbe
having potential for the bioremediation of environments
contaminated by aliphatic compounds. We have constructed
a BAC library for O. anthropi that provides a 90x genome
coverage based on an estimated genome size of 3.83 Mb.
The library contains 3072 clones with an average insert
size of 112 kbp. High-density colony filters of the
library were made and a physical map of the genome
constructed using a hybridization without replacement
strategy. In addition, 624 randomly chosen BAC clones
were HindIII fingerprinted and analyzed using Fingerprint
Contig (FPC; Sangre Centre, UK). The FPC results closely
supported and verified the hybridization contig data.
After determining a reduced tiling path of 69 clones,
138 BAC ends were sequenced for a genome wide survey of
gene distribution and gene structure."

FEATURES
source
1..577
/organism="Ochrobactrum anthropi"
/mol_type="genomic DNA"
/db_xref="taxon:529"
/clone="3P02-39r"
/lab_host="DH10B E. coli"
/clone_lib="Ochrobactrum anthropi BAC Library"
/note="Vector: pBelosAC11; Site 1: HindIII; Site 2:
HindIII; Ochrobactrum anthropi is an important microbe
having potential for the bioremediation of environments
contaminated by aliphatic compounds. We have constructed
a BAC library for O. anthropi that provides a 90x genome
coverage based on an estimated genome size of 3.83 Mb.
The library contains 3072 clones with an average insert
size of 112 kbp. High-density colony filters of the
library were made and a physical map of the genome
constructed using a hybridization without replacement
strategy. In addition, 624 randomly chosen BAC clones
were HindIII fingerprinted and analyzed using Fingerprint
Contig (FPC; Sangre Centre, UK). The FPC results closely
supported and verified the hybridization contig data.
After determining a reduced tiling path of 69 clones,
138 BAC ends were sequenced for a genome wide survey of
gene distribution and gene structure."

ORIGIN
Query Match
26.1%; Score 126.4; DB 28; Length 577;

```

```

Best Local Similarity 54.5%; Pred. No. 5.4e-23;
Matches 253; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

QY 1 ATGCGAATTGGACACGGTTTTCAGCTAATGCTTTGGGGTGAAGGCCCAATTATCATTT 60
Db 65 ATTCTACTGGCAATGGTTATGACGTCATTCCTTTTGAACCCGGCATCATGTGACGCTG 124
QY 61 GTTGGCGTACGATTCCTTACGAAAGGATGCTGGCGCATCTCTGATGGCGACGCTGGCG 120
Db 125 TGCAGTGTGAAATTTCCCAACGAAAGCAACTCAATGGCCATTCAGACCCCATGTTGA 184
QY 121 CTCCTATGCTTACCGATGATCTTGTGGCGGGGGCGCTGGGGGATATCGGCAAGCTG 180
Db 185 CTTTATGACTACGACGCGCTTGTGGACGCGAGGAGCGGATATCGGACGCAAT 244
QY 181 TTCCCGGATACGATTCGGCATTTAAAGTTCGCGATAGCCGCGAGCTGTACGCGAGCC 240
Db 245 TTCCCGCTTCGACCCCAATGAAAGCGCTGTTCCTCCGCATCTTTATCGAATGCT 304
QY 241 TGGCGTCTGATTACGCGAGGATTTATACCTTGGCAAGTGTGATCTACTATCATCGCT 300
Db 305 GCCAATATCGTGGTGAAGCTGGCGGTGTATGCGCAATGTGACGTGACCTTTATCAGC 364
QY 301 CAGGACCGAAGATGTGCGGCACATTCACAAATCGCGCTGTTTATTCGCGAAGATCTC 360
Db 365 GAAGACCGAAGATCGGCCACATCGTGACGAATGACGGAAGCTCTTTGCGACATGCTG 424
QY 361 GCGTGCATATGATGATGTTAACTGTAAGCAAGCCACTACTACGGAAGAACTGGGATTTAC 420
Db 425 GGAATTTCCCGCGATCGCTTTTCATCAAGCGACACCAATGAAAGCTGGGCTTCGTC 484
QY 421 GCACTGGGAGGAGTTCCTGTGAAGCGGTGGCGCTACTCAT 464
Db 485 GGAAGCGGTGAAGGATCGTGCCTATGCAAGCGCAACCGTCAT 528

RESULT 10
BF633873/c
LOCUS
DEFINITION
5', mRNA sequence.
ACCESSION
BF633873
VERSION
BF633873.1 GI:11898031
KEYWORDS
EST.
SOURCE
Medicago truncatula (barrel medic)
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 305)
Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula drought library
Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 305 Std Error: 0.00
Plate: 072 row: A column: 05
Seq primer: TCACAGGAAACAGCTATGAC.
Location/Qualifiers
1..305
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF072A05DT"
/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/clone_lib="Drought"

FEATURES
source
1..305
Query Match 25.4%; Score 123; DB 10; Length 305;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
QY 362 GCTGCCATATGATGATGTTAACTGTAAGCGGTGGCGCTACTCATTAAAGCAACAAAATGAT 481
Db 305 GCTGCCATATGATGATGTTAACTGTAAGCGGTGGCGCTACTCATTAAAGCAACAAAATGAT 246
QY 422 GACGTGGGAGGAGTTCCTGTGAAGCGGTGGCGCTACTCATTAAAGCAACAAAATGAT 481
Db 245 GACGTGGGAGGAGTTCCTGTGAAGCGGTGGCGCTACTCATTAAAGCAACAAAATGAT 186
QY 482 TGA 484
Db 185 TGA 183

RESULT 11
BF634326/c
LOCUS
DEFINITION
305 bp mRNA linear EST 19-DEC-2000
NF074G12DT1F1099 Drought Medicago truncatula cDNA clone NF074G12DT
5', mRNA sequence.
ACCESSION
BF634326
VERSION
BF634326.1 GI:11898484
KEYWORDS
EST.
SOURCE
Medicago truncatula (barrel medic)
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 305)
Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula drought library
Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 305 Std Error: 0.00
Plate: 074 row: G column: 12
Seq primer: TCACAGGAAACAGCTATGAC.
Location/Qualifiers
1..305
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF074G12DT"
/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/clone_lib="Drought"

FEATURES
source
1..305
Query Match 25.4%; Score 123; DB 10; Length 305;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
QY 362 GCTGCCATATGATGATGTTAACTGTAAGCGGTGAAGCCACTACTACGGAAGAACTGGGATTTACCG 421

```

```

Db      305  GCTGCCATATGATGATGTTAACTGTAAGAGCCACTACTACGGAATACTGGGATTTACCG 246
|||
Qy      422  GACGTGGGGAAGGATTCCTGTGAAGCGGTGGCGCTACTCATTAAGGCAACAATATGAT 481
|||
Db      245  GACGTGGGGAAGGATTCCTGTGAAGCGGTGGCGCTACTCATTAAGGCAACAATATGAT 186
|||
Qy      482  TGA 484
|||
Db      185  TGA 183
|||

RESULT 12
BI873743
LOCUS
DEFINITION
963110H07.y1 C. reinhardtii CC-1690, Stress condition I,
normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA
sequence.
BI873743
BI873743.1 GI:16071747
EST.
SOURCE
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 642)
Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C.,
Lefebvre, P., McDermott, J.P., Shrago, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Uncellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 963
Unpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.

FEATURES
source
1..642
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress condition I,
normalized, Lambda Zap II"
/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP-N (30 min, 1hr, 4hr), TAP-S (30 min,
1hr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30min,
1hr, 4hr) and NH4 to NO3 (30min, 1hr, 4hr). PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda Zap II
(Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exassist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

ORIGIN
Query Match 25.3%; Score 122.4; DB 12; Length 642;
Best Local Similarity 54.0%; Pred No. 6.7e-22;
Matches 249; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

Qy      4 CGAATTGACACGGTTTTCAGTACATCCCTTTGGCGGTGAAGGCCCAATTATCATTCGTT 63
|||
Db      142  CGCGTTGGCGACGGCTTTGACTGTCACCGCTGGCGGAGGGGTACAACCTCATTAATTGGC 201
|||

Qy      64  GCGGTACGCATTCCTTACAAAAGGATTGCTGGCGCATTCGTATGGCGAGTGGCGGCTC 123
|||
Db      202  GGTATCGACATCCCCACACCAAGGGCTGCGAGGGCCCACTCCGATGGCGAGTGTGCTG 261
|||

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Qy      124  CATCGTTACCGATGCATTGCTTGGCGGGCGCGCTGGGGATATCGGAAGCTGTTTC 183
|||
Db      262  CACACGTTGACGAGCGCTATCTCGCGCTGTGTGCTCCAGACATCGCGCAGCTGTTTC 321
|||
Qy      184  CCGGATACCGATTCGGCATTTTAAAGGTGCGGAGCTAGCCGGAGCTGCTACGCGAAGCTGG 243
|||
Db      322  CCAGACACGAGCCCAAGTGGGAAGGGCGCCCTCGGACATCTTCTTAAGAGGGCGTTC 381
|||
Qy      244  CCGCTATTTCAGCGGAAGGGTTATACCCCTTGGCAACGTCGATGTCACCTATCATCGTCTAG 303
|||
Db      382  CGGCTGATGGATGAGAAGGGTTACCTGCTGGGGAACCTGCACTGCACCATCATCGCGCAG 441
|||
Qy      304  GCACCGAAGATGTTGCGCGCACATTCACAAATGCGCGTGTATTATTCGCCGAAGATCTCGGC 363
|||
Db      442  AAGCCCAAGCTGTCCGCCCAAGAGGAGAACATCCGCAACAACCTGAGTGCCATCTCTGGGC 501
|||
Qy      364  TGCCATATGGATGATGTTAAAGTGAAGCACTACTACGGAATACTGGGATTTACCGGA 423
|||
Db      502  GCTGACCCCTCGTGTGTCACATCAAGGCCAAGACGCGAGAGAGGTGATAGCTGNGC 561
|||
Qy      424  CCGTGGGAAGGATTCCTGTGAAGCGGTGGCGCTACTCAT 464
|||
Db      562  GAGGAGCGCTCCATCGCTGCCACGCCGTGGTGTGATCTTAT 602
|||

RESULT 13
BU238300
LOCUS
DEFINITION
Ds01_15m07 A Ds01 AAPC ECORC cold stressed Flixweed seedlings
Descurainia sophia cDNA clone Ds01_15m07, mRNA sequence.
BU238300
BU238300.1 GI:22750125
EST.
SOURCE
Descurainia sophia
Descurainia sophia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Descurainia.
1 (bases 1 to 773)
Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J.,
Hattori, J.I., Ouellet, T., Robert, L.S., Spiro, D. and Tinker, N.A.
Expressed Sequence Tags from Cold-Stressed Descurainia sophia
Seedlings
Unpublished (2001)
Contact: Singh, J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA
OC6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
Location/Qualifiers
1..773
/organism="Descurainia sophia"
/mol_type="mRNA"
/db_xref="taxon:89411"
/clone="Ds01_15m07"
/tissue_type="leaf, stem"
/dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
/gs="
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI;
Site 2: Xho I; Plants were grown for 1 month at 20oC/16
hrs light/day (average 8 leaves, 1 cm tall, weight
0.02g/plant). Then they were exposed to 2oC, 12 hrs
light/day, for 1 week. Library prepared by C. Piche using
Stratagene kit."

ORIGIN
Query Match 25.0%; Score 121; DB 13; Length 773;
Best Local Similarity 53.5%; Pred. No. 1.7e-21;

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Matches	250;	Conservative	1;	Mismatches	216;	Indels	0;	Gaps	0;
Qy	2	TGCGAATTGACACGGTTTTGAGCTACATGCCCTTTGGCGGTGAAGGCCCAATTATCATTTG	61						
Db	226	TTTCAATCGTTCACGGTTTCGATCTACATCGTTAGAGCCAGGATACCCCTCTGATCATCG	285						
Qy	62	GTGCGGTACGCATTCCTTAGAAAAGGATTGTTGGCGCATTCGTAGTGGCGACGTGGCGC	121						
Db	286	GCGGGATGATATTCCTCACGATAGAGGCTGCGAAGCTCACTCCGATGGCGGATGTGTGC	345						
Qy	122	TCCATCGTTGACCGATGCATTCGTTGGCGCGCGCGCTGGGGGATATCGGCAAGCTGT	181						
Db	346	TTTCAATTCGTAGTGCATGCAATTTTGGAGCATTTAGGGCTTCTTGATATAGTCCAGATTT	405						
Qy	182	TCCCGGATACCGATTCGGCATTTTAAAGTGTCCGATAGCCGGAGCTCGTAGCGAAGCTT	241						
Db	406	TCCTGTATTCGTATCTCTAAATGGAAGAGAGTGTCTTCTGTGTTTTTCATCAAGAAGCTG	465						
Qy	242	GGCGTTCGATTCAGGCGCAAGGGTTATACCTTTGGCAACGTCGATGTCACTATCATCGCTC	301						
Db	466	TGAGACTAATGAACGTGGCAGGGTACAGATASGAACCTAGACGCAACTGATTCCTC	525						
Qy	302	AGCACCGAAGATGTTGCGGCACATTCACAAATTCGGGTGTTTATTGCGCAAGATCTCG	361						
Db	526	AGAGACCAAGATAAAGTCTCACAAAGGAGACAATCCGAYCCAACTCTGTCCAAGCTTCTTG	585						
Qy	362	GCTGCCATATGGATGATGTTAACTGTAAGGCACTACTACGGAAGAACTCGGATTTACCG	421						
Db	586	GAGCTGATCCTTCTGTTGTGNACTTAAAGCCAAACACATGAGAAAGTTGATAGCCTCG	645						
Qy	422	GACGTGGGAAGGATTCCTGTGAAAGCGGTGGCGCTACTCATTAAG	468						
Db	646	GAGAAACAGAAGCATTCGAGCTCACACTGTTATTCTCTCATGAAG	692						

